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Original Article

Bacteria isolated from blood cultures in a neonatal and pediatric intensive care unit and their antibiotic resistance: 5-year results

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ABSTRACT

Objective: Bloodstream infections represent a leading cause of illness and death among children in developing nations. The aim of this study was to determine the bacterial profile and antibiotic resistance status of pathogens isolated from blood cultures taken from children in the neonatal and pediatric intensive care units of a university hospital in Türkiye.

Methods: Isolation, species identification, and antibiotic susceptibility testing of 1,197 blood culture samples from the neonatal and pediatric intensive care units of a university hospital were conducted using classical methods and automated Bact Alert and BD Phoenix systems between January 2018 and December 2022.

Results: Of the 1197 blood cultures included in the study, 776 (64.82%) were isolated from neonatal, and 421 (35.18%) were isolated from the pediatric intensive care unit. Of the 1197 microorganisms identified in blood cultures, 868 (72.51%) were gram-positive, 259 (21.63%) were gram-negative bacteria, and 70 (5.84%) were fungi. Among the identified bacteria, the most common microorganism was coagulase-negative staphylococci (62.40%), followed by *Klebsiella pneumoniae* (6.59%) and *Acinetobacter baumannii* (6.26%). Methicillin resistance was 93.44% in coagulase-negative staphylococci and 54.54% in *Staphylococcus aureus*. Among Gram-negative bacteria, *Acinetobacter baumannii* showed a high resistance to all antibiotics tested, while *Serratia marcescens* had the highest susceptibility rate.

Conclusion: According to the results of our study, the antibacterial resistance rates of microorganisms isolated from blood cultures differ. We believe that regular monitoring of susceptibility patterns of strains will encourage rational antibiotic use and provide more effective treatment by reducing resistance among bacteria.

Keywords: antibiotic resistance, child, intensive care units, neonatal, Türkiye

INTRODUCTION

Bloodstream infections are quite common in the pediatric age group and are a significant cause of morbidity and mortality, particularly in neonates and children. These infections pose a life-threatening risk, especially in immunocompromised patients admitted to intensive care units (ICUs).[1] Globally, bloodstream infections affect approximately 30 million people annually, resulting in 6 million deaths.[2] Every year, 3 million neonates and 1.2 million children suffer from sepsis, leading to serious health issues.[3]

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In ICUs, Gram-positive microorganisms are most frequently isolated from blood cultures. Among them, *coagulase-negative staphylococci* (*CoNS*) are the most common, followed by *Staphylococcus aureus* (*S. aureus*) and *Enterococcus* species.[4,5] Gram-negative bacteria, such as *Acinetobacter* species, *Escherichia coli* (*E. coli*), *Pseudomonas aeruginosa* (*P. aeruginosa*), *Klebsiella pneumoniae* (*K. pneumoniae*), and *Haemophilus influenzae* (*H. influenzae*), are also frequently isolated.[1,5]

The identification of bloodborne pathogens and the determination of their antibiotic susceptibility are urgent medical priorities.[6] However, since bacteriological cultures and susceptibility testing take several days, empirical antimicrobial treatment is typically initiated before blood culture results are available in nearly all cases.[7] A major issue associated with empirical therapy is the emergence of antibiotic resistance.[8] The increasing antimicrobial resistance in bloodstream infections, particularly in developing countries, is a growing concern, and studies conducted in these regions have reported a rise in antibiotic resistance.[9-12] Rational and appropriate use of antibiotics requires knowledge of the most commonly isolated bacteria from blood cultures and their antibiotic susceptibility patterns.[13] Early detection of antimicrobial susceptibility patterns has been shown to reduce morbidity and mortality associated with bloodstream infections.[14]

The aim of this study is to determine the bacterial profile and antibiotic resistance status of pathogens isolated from blood cultures of children admitted to neonatal and pediatric intensive care units of a university hospital in Türkiye over a five-year period.

MATERIAL AND METHODS

Study design

This study is a retrospective evaluation of approximately 1,197 blood cultures sent from neonatal and pediatric ICUs to the Medical Microbiology Laboratory of a university-affiliated Health Application and Research Hospital.

Study population and sample

The study includes blood culture results from patients admitted to neonatal and pediatric intensive care units between January 1, 2018, and December 31, 2022. The hospital where the study is conducted has a 39-bed neonatal intensive care unit (5 at level 1, 17 at level 2, and 17 at level 3) and a 15-bed pediatric intensive care unit (5 at level 2 and 10 at level 3). These units serve as a center with a high volume of cases involving anomalies, chronic diseases, and post-surgical patients. Patients without blood culture data were excluded from the study.

Data collection tools

The data regarding blood culture results were obtained through a retrospective review of patient records. Microorganisms were identified using conventional methods and the Phoenix automated system (Becton Dickinson, Sparks, Maryland, USA). Antibiotic susceptibility results were evaluated according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) criteria.[15]

This study was approved by the Kahramanmaraş Sütçü İmam University Medical Research Ethics Committee (approval date 12.09.2023, number 2023/13-03).

Statistical analysis

Statistical analyses were performed using the SPSS software version 22 (IBM Corp. Released 2010. IBM SPSS Statistics for Windows, Version 22.0. Armonk, NY: IBM Corp.). Categorical data were presented with n and %.

RESULTS

Over the course of five years, 6,291 blood cultures were collected from neonatal and pediatric intensive care units, with microbial growth detected in 1,197 samples (19.02%). Of the microorganisms isolated, 621 (51.88%) were from male and 576 (48.12%) from female patients. Among the 1,197 cultures with growth, 776 (64.82%) were obtained from neonatal ICUs, while 421 (35.18%) were from pediatric ICUs.

Among the 1,197 microorganisms isolated, 868 (72.51%) were identified as Gram-positive bacteria, 259 (21.63%) as Gram-negative bacteria, and 70 (5.84%) as *Candida* species. The most frequently isolated microorganism was *CoNS (62.40%)*, followed by *K. pneumoniae* (6.59%), *A. baumannii* (6.26%), *Candida parapsilosis (C. parapsilosis)* (3.17%), and *Enterococcus faecalis (E. faecalis)* (2.08%). The distribution of microorganisms isolated from blood cultures is shown in Table 1.

Table 1. Bacteria isolated from blood cultures		
Gram-Positive Bacteria	**868**	**72.51**
***Staphylococcus* spp.**	**770**	**64.32**
Staphylococcus aureus	23	1.92
Coagulase Negative Staphylococci	747	62.40
***Streptococcus* spp.**	**29**	**2.42**
Streptococcus mitis	9	0.75
Streptococcus oralis	8	0.66
Other streptococci		
Streptococcus pneumoniae, Streptococcus acidominimus Streptococcus constellatus, Streptococcus oralis, Streptococcus cristatus, Streptococcus gallolyticus, Streptococcus sanguinis, Streptococcus salivarius, Streptococcus parasanguinis, Streptococcus vestibularis	12	1.00
Other Gram-Positive Bacteria	**6**	**0.50**
Aerococcus viridans Leuconostos lactis, Listerıa monocytogenes, Gemella morbillorum, Pediococcus pentosaceus, Rothia dentocari-osa	6	0.50
***Enterococcus* spp.**	**49**	**4.09**
Enterococcus faecalis	25	2.08
Enterococcus faecium	20	1.67
Other enterococci (*Enterococcus avium, hirae, raffinosus, casseliflavus / gallinarum*)	4	0.33
***Corynebacterium* spp.**	**14**	**1.16**
Corynebacterium amycolatum/minutissimum	4	0.33
Corynebacterium jeikeium	4	0.33
Corynebacterium matruchotii	2	0.16
Other Corynebacteria *(bovis, pseudodiphtheriticum, amycolatum, striatum)*	4	0.33
Gram-Negative Bacteria	**259**	**21.63**
***Klebsiella* spp.**	**88**	**7.35**
Klebsiella pneumoniae	79	6.59
Klebsiella oxytoca	6	0.50
Other Klebsiella species *(Klebsiella ozaenae, aerogenes)*	3	0.25
***Serratia* spp.**	**18**	**1.50**
Serratia marcescens	18	1.50
Escherichia coli	**15**	**1.25**
***Enterobacter* spp.**	**9**	**0.75**
Enterobacter cloacae	8	0.66
Enterobacter aerogenes	1	0.08
***Proteus* spp.**	**2**	**0.16**
***Pseudomonas* spp.**	**19**	**1.58**
Pseudomonas aeruginosa	18	1.50
Pseudomonas putida	1	0.08
***Acinetobacter* spp.**	**78**	**6.51**
Acinetobacter baumannii	75	6.26
Acinetobacter lwoffii / haemolyticus	3	0.25
***Bacillus* spp.**	**6**	**0.50**
Bacillus cereus	2	0.16
Bacillus pumilus	4	0.33
Other gram-negative bacteria	**24**	**2.00**
Stenotrophomonas maltophilia	9	0.75
Other bacteria *(Morganella morganii, Pantoea agglomerans, Brevundimonas diminuta, Burkholderia cepacia complex, Rhizobium radiobacter, Chryseobacterium meningosepticum)*	15	1.25
***Candida* spp.**	**70**	**5.84**
Candida albicans	20	1.67
Candida parapsilosis	38	3.17
Other candidas (*candida lusitaniae /tropicalis / kefyr / glabrata*)	12	1.00
Total	1197	100

Table 2. Antibiotic resistance rates of gram-positive bacteria isolated from blood cultures

Antibiotics	*S. aureus*		*CoNS		*Enterococcus* spp.		*Streptococcus* spp.	
	n	**R (%)**	**n**	**R (%)**	**n**	**R (%)**	**n**	**R (%)**
Ampicillin	-	-	554	552 **(99.63)**	45	18 (40.00)	-	-
Clindamycin	22	9 (40.90)	747	556 (74.43)	-	-	9	3 (50.00)
Daptomycin	22	1 (4.54)	747	16 (2.14)	-	-	1	**0 (0.00)**
Erythromycin	23	10 (43.47)	747	664 (88.88)	-	-	4	3 (75.00)
Fusidic Acid (STAFINE)	23	2 (8.69)	747	452 (60.50)	-	-	-	-
Gentamicin	22	3 (13.63)	747	586 (78.44)	-	-	1	1 **(100)**
Levofloxacin	22	4 (18.18)	747	540 (72.28)	-	-	3	0 **(0.00)**
Linezolid	23	1 (4.34)	747	16 (2.14)	45	0 **(0.00)**	5	0 **(0.00)**
Oxacillin	22	12 **(54.54)**	747	698 (93.44)	-	-	-	-
Ciprofloxacin	22	4 (18.18)	747	548 (73.36)	-	-	-	-
Teicoplanin	23	2 (8.69)	722	89 (12.32)	45	10 (22.22)	11	**0 (0.00)**
Tetracycline	23	6 (26.08)	747	210 (28.11)	-	-	3	2 (66.66)
Trimethoprim/sulfamethoxazole	23	1 (4.34)	676	159 (23.52)	30	30 **(100)**	3	2 (66.66)
Vancomycin	23	**0 (0.00)**	747	6 **(0.80)**	45	11 (24.44)	13	**0 (0.00)**
HLGR **	-	-	-	-	45	20 (44.44)	8	2 (25.00)
HLSR ***	-	-	-	-	45	16 (35.55)	-	-

**CoNS*: coagulase-negative staphylococci, **HLGR: High-Level Gentamicin Resistance, ***HLSR: High-Level Streptomycin Resistance, R: Resistance
- Indicates that antibiotics have not been tested against this organism.

Among *CoNS* isolates, the highest resistance was observed against ampicillin (99.63%), oxacillin (93.44%), and erythromycin (88.88%). The lowest resistance was found against vancomycin (0.80%), linezolid (2.14%), and daptomycin (2.14%). In *S. aureus* isolates, the highest resistance was noted against oxacillin (54.54%), erythromycin (43.47%), and clindamycin (40.90%). No resistance to vancomycin was detected in *S. aureus* isolates, while the lowest resistance was observed against linezolid (4.34%) and daptomycin (4.54%). *Enterococcus* species showed 100% resistance to trimethoprim/sulfamethoxazole, with no resistance detected to linezolid. Among *Streptococcus* species, the highest resistance was observed against erythromycin (75%), while no resistance was detected to vancomycin, teicoplanin, linezolid, levofloxacin, or daptomycin. Antibiotic resistance rates for Gram-positive bacteria are presented in Table 2.

Among Gram-negative bacteria, *Klebsiella* species, *Serratia marcescens* (*S. marcescens*), and *Enterobacter cloacae* (*E. cloacae*) isolates demonstrated the highest resistance to ampicillin, with a 100% resistance rate. The ampicillin resistance rate for *E. coli* was 85.71%. *A. baumannii* was identified as the most resistant bacterium, with resistance rates exceeding 90% for most antibiotics tested, except trimethoprim/sulfamethoxazole. The second-highest resistance rates were found in *Klebsiella* species, while the lowest resistance rates were observed in *S. marcescens* and *E. cloacae* isolates. The highest carbapenem resistance was found in *A. baumannii*, followed by *Klebsiella* species, *Pseudomonas*, and *E. cloacae*. Antibiotic resistance rates for Gram-negative bacteria are shown in Table 3.

In *Candida albicans (C. albicans)* isolates the highest antifungal resistance was observed against voriconazole (85.00%). In contrast, in *C. parapsilosis* isolates, the highest resistance was observed against fluconazole (24.24%). No resistance to caspofungin was detected in either *Candida* species. Antifungal resistance rates for *Candida* species are presented in Table 4.

Table 3. Antibiotic resistance rates of gram-negative bacteria isolated from blood cultures

Antibiotics	*Klebsiella spp.*		*Serratia marcescens*		*E. coli*		*Pseudomonas aeruginosa*		*Acinetobacter spp.*		*Enterobacter cloacae*	
	n	**R (%)**	**n**	**R (%)**	**n**	**R (%)**	**n**	**R (%)**	**n**	**R (%)**	**n**	**R (%)**
Amikacin	84	36 (42.85)	18	2 (11.11)	15	1 **(6.66)**	18	2 **(11.11)**	74	69 (93.24)	8	2 **(25.00)**
Gentamicin	85	45 (52.94)	18	1 (5.55)	15	3 (20.00)	8	1 (12.50)	75	72 **(96.00)**	8	3 (37.50)
Ciprofloxacin	80	50 (62.5)	18	0 **(0.00)**	13	1 (7.69)	18	6 (33.33)	73	69 (94.52)	8	2 **(25.00)**
Levofloxacin	58	31 (87.93)	9	0 **(0.00)**	12	1 (8.33)	13	7 (53.84)	53	49 (92.45)	6	2 (33.33)
Ampicillin	84	84 **(100)**	18	18 **(100)**	14	12 **(85.71)**	-	-	-	-	8	8 **(100)**
Ertapenem	85	64 (75.29)	18	6 (33.33)	14	1 (7.14)	-	-	-	-	7	3 (42.85)
Imipenem	84	27 **(32.14)**	18	6 (33.33)	14	1 (7.14)	18	13 **(72.22)**	75	71 (94.66)	8	2 **(25.00)**
Meropenem	84	44 (52.38)	17	2 (11.76)	15	1 (6.66)	18	7 (38.88)	75	71 (94.66)	8	3 (37.50)
Ceftriaxone	85	71 (83.52)	18	2 (11.11)	14	6 (42.85)	-	-	-	-	8	2 **(25.00)**
Cefuroxime	83	71 (85.54)	-	-	14	9 (64.28)	-	-	-	-	-	-
Cefepime	83	70 (84.33)	18	1 (5.55)	15	4 (26.66)	17	7 (41.17)	-	-	7	2 (28.57)
Ceftazidime	84	71 (83.52)	18	0 **(0.00)**	15	7 (46.66)	18	7 (38.88)	-	-	7	2 (28.57)
Piperacillin/tazobactam	84	66 (78.57)	18	5 (27.77)	15	4 (26.66)	18	5 (27.77)	-	-	8	2 **(25.00)**
Trimethoprim/sulfamethoxazole	85	58 (68.23)	18	0 **(0.00)**	14	6 (42.85)	-	-	75	40 **(53.33)**	8	2 **(25.00)**

- Indicates that antibiotics have not been tested against this organism.

Table 4. Antifungal resistance rates of Candida isolated from blood cultures

Antifungals	*Candida albicans*		*Candida parapsilosis*	
	n	**R (%)**	**n**	**R (%)**
Voriconazole	20	17 **(85.00)**	33	1 (3.03)
Caspofungin	20	0 **(0.00)**	33	0 **(0.00)**
Fluconazole	20	8 (40.00)	33	8 **(24.24)**
Amphotericin-B	20	3 (15.00)	33	6 (18.18)

DISCUSSION

The 19.02% culture positivity rate observed in this study is consistent with findings from previous research on the subject. For instance, Deku et al.[16] reported a culture positivity rate of 13.1% in Ghana, Gupta et al.[17] found 16.5% in North India, and Oyekale et al.[18] reported 19.2% in Nigeria. However, some studies have reported lower rates, including Khanal et al.,[19] Gohel et al.,[20] and Gülmez et al.[21] who documented culture positivity rates of 10.3%, 9.2%, and 7.7%, respectively, in bloodstream infection cases.

Gram-positive bacteria were the most frequently isolated strains from blood cultures, followed by gram-negative bacteria and candida.[22] In this study, gram-positive bacteria were found to be the predominant strains (72.51%) (Table 1). This finding aligns with prior studies, which have also reported Gram-positive bacteria as the dominant isolates in bloodstream infection cases.[16,23] However, some research has highlighted Gram-negative bacteria as the most frequently isolated pathogens in bloodstream infections.[17,18]

Although the importance and role of *CoNS* as etiological agents of neonatal sepsis have been proven in many studies, determining whether *CoNS* isolates are true pathogens or contaminants remains problematic.[24] In this study, *CoNS* was the most frequently isolated microorganism (62.40%), followed by *Enterococcus* spp. (4.09%). This result is consistent with the findings of Ergül et al.[22] The high isolation rate of *CoNS* may be attributed to the frequent invasive procedures performed on patients.

The prevalence of *S. aureus* in blood cultures varies across different studies. For example, *S. aureus* rates of 42.39% in Pakistan[25], 40.72% in India[26], 11.95% in Afghanistan[27], and 8.87% in Iran[7] have been reported, while lower rates (0.9-12.8%) have been observed in Türkiye.[21,22,28,29] The isolation rate of *S. aureus* in our study (1.92%) is consistent with the rates reported in Türkiye.

In our study, in addition *to CoNS, Klebsiella, Acinetobacter, S. aureus, Enterobacter, E. coli, Pseudomonas, Streptococcus, Serratia*, and *candida* species were isolated (Table 1). These findings are consistent with previous studies[22,27,30] and it has been reported that infections caused by these bacteria pose a significant threat to the lives of children.[27]

In our study, the methicillin resistance rate in *CoNS* was found to be significantly higher compared to *S. aureus* (*CoNS* 93.44%, *S. aureus* 54.54%) (Table 2). Similar findings have also been reported in several studies conducted in Türkiye.[22,28] In this study, which evaluated five years of data, no vancomycin resistance was detected in *S. aureus*. In contrast, vancomycin resistance rates in *CoNS* and *enterococci* were found to be 0.80% and 24.44%, respectively. The resistance rates for teicoplanin were determined to be 8.69%, 12.32%, and 22.22%, while linezolid resistance was 4.34% in *S. aureus* and 2.14% in *CoNS* (Table 2). Previous studies have reported higher susceptibility to vancomycin, teicoplanin, and linezolid.[26,31]

In our study, the most frequently isolated gram-negative bacteria were *Klebsiella* spp. (7.35%), followed by *Acinetobacter* spp. (6.51%) (Table 3). This finding contrasts with reports from a study in Western India, where *Acinetobacter* spp. was the most frequently isolated bacterium, followed by *Klebsiella* spp.[31] Additionally, similar studies have shown variability in bacterial ranking.[6,22,25,27] *Klebsiella* spp isolated in our study showed high levels of resistance to most of the tested antibiotics. Specifically, the antibiotics to which *Klebsiella* spp. showed the highest resistance were ampicillin (100%), cefuroxime (85.54%), cefepime (84.33%), and ceftriaxone (83.52%) (Table 3). These results are consistent with other studies.[6,22] Our study suggests that the high aminoglycoside and cephalosporin resistance observed in *Klebsiella* strains may be due to the inappropriate use of these antibiotics in empirical treatment.

Acinetobacter spp. has shown high levels of resistance to all tested antibiotics (Table 3). Consistent with our findings, Shehab El-Din et al.[24] reported even higher resistance rates. Moradi et al.[11] also found results similar to ours, although they reported still high antibiotic resistance. In contrast, Maham et al.[7] presented lower antibiotic resistance rates for *A. baumannii* than our study. The high resistance observed in *Acinetobacter* species to various antibiotics has led to colistin and tigecycline becoming important treatment options.[22]

In this study, among the bacteria isolated from blood cultures, *S. marcescens*, which was isolated at a rate of 1.50%, was identified as the bacterium with the highest sensitivity rate to the tested antibiotics (excluding ampicillin) (Table 3). However, Shehab El-Din et al.[24] reported higher resistance rates for *S. marcescens* than our findings. This discrepancy may be attributed to Shehab El-Din et al.[24] isolating *S. marcescens* more frequently (7.17%) from blood cultures, which suggests that they may have used antibiotics more often in treating infections caused by this pathogen.

P. aeruginosa was isolated at a rate of 1.50%, and the most resistant antibiotic was imipenem, with a resistance rate of 72.22%, followed by levofloxacin, with a resistance rate of 53.84%. The most sensitive antibiotic was amikacin, with a resistance rate of 11.11%, followed by gentamicin, with a resistance rate of 12.50% (Table 3). Our study is consistent with the study of Akman et al.,[29] in which they found the resistance rates of amikacin (14.8%) and gentamicin (24.1%) to be lower than the resistance rate of imipenem (66.6%). However, Maham et al.[7] reported resistance rates (amikacin 37.1%, gentamicin 69.0%, imipenem 21.6%), contrary to our study. In this study, high carbapenem (66.6%) and quinolone resistance (53.84%) observed in *P. aeruginosa* strains may be related to inappropriate antibiotic use in empirical treatment. According to our results, aminoglycosides and ciprofloxacin may be preferred before carbapenems and quinolones in empirical treatment in patients with suspected *Pseudomonas* infection.

In our study, 1.25% of *E. coli* was isolated from blood cultures (Table 3). Khan et al.[25] isolated *E. coli* strains from blood cultures at a rate similar to our study (1.09%). However, in a study conducted by Fox-Lewis et al.[32], the percentage of *E. coli* was reported to be 47.2%, while a study conducted in Pakistan reported this percentage as 5%.[33] In our study, *E. coli* strains showed resistance rates of 85.71% to ampicillin, 64.28% to cefuroxime, and 20% to gentamicin; resistance rates for other tested antibiotics remained below 10%. The literature reports varying resistance rates for *E. coli*; for instance, Khan et al.[25] indicated that *E. coli* strains were susceptible to amikacin but highly resistant to imipenem and cefepime. Fox-Lewis et al.[32] did not detect carbapenem resistance, but they found gentamicin resistance to be approximately 45% and ampicillin resistance to be over 90%. Er et al.[34] reported low resistance rates for imipenem, meropenem, and amikacin while noting high resistance to cephalosporins and quinolone antibiotics. These differences may be related to the diversity of microorganisms that are frequently isolated in the hospitals where the studies were conducted and the frequency of treatment practices associated with them.

In this study, *E. cloacae*, which was isolated at a rate of 0.66% and has the highest antibiotic susceptibility after *S. marcescens* (excluding ampicillin), shows antibiotic resistance rates generally around 25% and slightly above (Table 3). However, various resistance rates have been reported in studies conducted in different countries and geographical regions.[24,29]

In recent years, there has been a significant increase in the isolation of *Candida* species in blood cultures due to the rise in occurrences of neutropenia, preterm birth, surgical procedures, and the use of intravascular catheters.[21] In this research, 5.84% of positive blood cultures were identified as Candida (Table 4). Different Candida rates have been reported in studies: Khan et al.[25] 2.17%, Tariq et al.[27] 3.41%, Mokaddas et al.[8] 7%, Gülmez et al.[21] 10.8%, Kumar et al.[35] 21%. In our study, *C. parapsilosis* (3.17%) was the most frequently isolated fungal species (Table 4). These findings contradict reports indicating that *C. albicans* is the most commonly isolated fungal pathogen in neonatal ICUs.[22,28,35]

Limitations of the study

The fact that the broth microdilution method used to determine colistin sensitivity was not tested in our hospital during the periods when the data were collected is among the limitations of our study.

CONCLUSION

In conclusion, this study identified gram-positive bacteria isolated from blood cultures as the dominant strains, with *CoNS* being the most frequently isolated bacteria. Antibiotic resistance was observed at the highest rate in *A. baumannii*, while resistance rates vary according to bacterial species. Studies in the literature reveal that the types of microorganisms isolated from blood cultures and antibacterial resistance rates vary significantly among hospitals in different countries. The main factors contributing to the increase in antimicrobial-resistant bacteria include poor infection control practices and inappropriate antibiotic use. Restriction of unnecessary antibiotic use, promotion of rational use, and specific antibiotic use strategies such as combination antibiotic therapy may help control the development of resistance. In addition, it would be useful to update the bacteriological profile and antibiotic susceptibility pattern in blood cultures at regular intervals to ensure correct empirical treatment.

Ethical approval

This study has been approved by the Kahramanmaraş Sütçü İmam University Medical Research Ethics Committee (approval date 12.09.2023, number 2023/13-03).

Author contribution

Study conception and design: MeA, AK, ZO; data collection: BK, ÖK; analysis and interpretation of results: MuA, ÖK; draft manuscript preparation: ZO, AK. All authors reviewed the results and approved the final version of the article.

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Conflict of interest

The authors declare that there is no conflict of interest.

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